

1647

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RAW SEQUENCE LISTING

DATE: 11/21/2002

PATENT APPLICATION: US/09/602,597A

TIME: 10:20:07

#26

Input Set : A:\PP-01568.002 59516-159.ST25.txt

Output Set: N:\CRF4\11212002\I602597A.raw

p.6

3 <110> APPLICANT: Duhl, David
 4 Gorman, Susan W
 6 <120> TITLE OF INVENTION: HUMAN CHROMOSOME 16 PLASMOLIPIN-LIKE POLYPEPTIDE
 8 <130> FILE REFERENCE: PP-01568.002/59516-159
 10 <140> CURRENT APPLICATION NUMBER: US 09/602,597A
 11 <141> CURRENT FILING DATE: 2000-06-22
 13 <160> NUMBER OF SEQ ID NOS: 12
 15 <170> SOFTWARE: PatentIn version 3.1
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 2850
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Homo sapiens
 22 <220> FEATURE:
 23 <221> NAME/KEY: CDS
 24 <222> LOCATION: (214)..(978)
 25 <223> OTHER INFORMATION:

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33	agagcgagcg gctctgcggt ggcgggtttgg ggtgggcgcc gccgaggtga ggtcgtctcg	180
35	cctcccgcgc gccggtagat tgggtgtttc att atg gat gga ggg gat gat ggt	234
36		
37	Met Asp Gly Gly Asp Asp Gly	
39	aac ctt att atc aaa aag agg ttt gtg tct gag gca gaa cta gat gaa	282
40	Asn Leu Ile Ile Lys Lys Arg Phe Val Ser Glu Ala Glu Leu Asp Glu	
41	10 15 20	
43	cgg cgc aaa agg agg caa gaa gaa tgg gag aaa gtt cga aaa cct gaa	330
44	Arg Arg Lys Arg Arg Gln Glu Glu Trp Glu Lys Val Arg Lys Pro Glu	
45	25 30 35	
47	gat cca gaa gaa tgt cca gag gag gtt tat gac cct cga tct cta tat	378
48	Asp Pro Glu Glu Cys Pro Glu Glu Val Tyr Asp Pro Arg Ser Leu Tyr	
49	40 45 50 55	
51	gaa agg cta cag gaa cag aag gac agg aag cag cag gag tac gag gaa	426
52	Glu Arg Leu Gln Glu Gln Lys Asp Arg Lys Gln Gln Glu Tyr Glu Glu	
53	60 65 70	
55	cag ttc aaa ttc aaa aac atg gta aga ggc tta gat gaa gat gag acc	474
56	Gln Phe Lys Phe Lys Asn Met Val Arg Gly Leu Asp Glu Asp Glu Thr	
57	75 80 85	
59	aac ttc ctt gat gag gtt tct cga cag cag gaa cta ata gaa aag caa	522
60	Asn Phe Leu Asp Glu Val Ser Arg Gln Gln Glu Leu Ile Glu Lys Gln	
61	90 95 100	
63	cga aga gaa gaa gaa ctg aaa gaa ctg aag gaa tac aga aat aac ctc	570
64	Arg Arg Glu Glu Glu Leu Lys Glu Leu Lys Glu Tyr Arg Asn Asn Leu	

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65	105	110	115	
67	aag aag gtt gga att tct caa gag aac aag aag gaa gtg gaa aag aaa	618		
68	Lys Lys Val Gly Ile Ser Gln Glu Asn Lys Lys Glu Val Glu Lys Lys			
69	120 125 130 135			
71	ctg act gtg aag cct ata gaa acc aag aac aag ttc tcc cag gcg aag	666		
72	Leu Thr Val Lys Pro Ile Glu Thr Lys Asn Lys Phe Ser Gln Ala Lys			
73	140 145 150			
75	ctg ttg gca gga gct gtg aag cat aag agc tca gag agt ggc aac agt	714		
76	Leu Leu Ala Gly Ala Val Lys His Lys Ser Ser Glu Ser Gly Asn Ser			
77	155 160 165			
79	gtg aaa aga ctg aaa ccg gac cct gag cca gat gac aag aat caa gag	762		
80	Val Lys Arg Leu Lys Pro Asp Pro Glu Pro Asp Asp Lys Asn Gln Glu			
81	170 175 180			
83	ccc tca tcc tgc aag tct ctc gga aac acc tcc ctg agt ggc ccc tcc	810		
84	Pro Ser Ser Cys Lys Ser Leu Gly Asn Thr Ser Leu Ser Gly Pro Ser			
85	185 190 195			
87	atc cac tgc ccc tct gct gca gta tgt atc ggc atc ctc cca ggc ctg	858		
88	Ile His Cys Pro Ser Ala Ala Val Cys Ile Gly Ile Leu Pro Gly Leu			
89	200 205 210 215			
91	ggt gcc tac tct ggg agc agc gac tcc gag tcc agc tca gac agc gaa	906		
92	Gly Ala Tyr Ser Gly Ser Ser Asp Ser Glu Ser Ser Ser Asp Ser Glu			
93	220 225 230			
95	ggc acc atc aat gcc acc gga aag att gtc tcc tcc atc ttc cga acc	954		
96	Gly Thr Ile Asn Ala Thr Gly Lys Ile Val Ser Ser Ile Phe Arg Thr			
97	235 240 245			
99	aac acc ttc ctc gag gcc ccc tag tttctccgtc cctacacagg gagctcctcc	1008		
100	Asn Thr Phe Leu Glu Ala Pro			
101	250			
103	ccaagggtag atcggaccgt tcatgtctgcc tataggcatt atgtccctca aaaaaaaact	1068		
105	ccttttgctg catcctgtgt acaacatgac atttttaacc aatccaatct aaaaatgtgc	1128		
107	cagaatccac ctgtggcccg aatcgtgttt ggttcctctt tctactccac tgcagatgac	1188		
109	caaacctgtc ccgctgccac tttcctcact gatattggga ggagggaag gccagccga	1248		
111	agttccacta aaaatgcccc aggagaatag gcaccggctg gcttgccaaa gggtttgggt	1308		
113	tttattgctt tctgtttttt cttttcccga cagcacaag aagtaagggc agttattgga	1368		
115	cagggtgttat ttaaaccattc tattgtaaat gaatgtgtg tttggttcta ctgcattgtg	1428		
117	gagcatgcgg gggaagagaa ctgacccagg taatgaaatg gagcccttcc ctggaactaa	1488		
119	ccagtccttg atgttggtgt actaagtaaa gatgataaac cccatctgct gggggtgtca	1548		
121	cttcacactc ggcatgcatt gtgaaagctt tccataacct tggccattcc ctctctcctc	1608		
123	tctctccaac cccatttatg caggaaggga ctgctaacaa gaacgcttcc atctcaaacc	1668		
125	ttttctctgc ctgggaaatt attttatgtt tgtttttgaa ataaaggatt tagtttaaga	1728		
127	ttctaaattt tagagaaaca aacgtaggcc ttgtttacta atagccagac atcagaactg	1788		
129	caggtaggta tgtaaatgag atgacttatt tctggcagct cctggaatcc taatattgta	1848		
131	aatgagtggg acacactgc atattgtgac cattctattg aggcctctc tgtttaatgc	1908		
133	atattatact tgtgctttta actgtggaat ctatttctaa cctaaagggtg ctgccctagt	1968		
135	acttttcttt gctgcctctg ctgctctttt tcttttccaa acagcaactc tgaggccatg	2028		
137	agcagccaaa aactagaggt actgctccac ctctgtctcat aaagggaac gggctcatcc	2088		
139	cttggaattc ggaggaggga gagggagatg gtgtggaggc ctcgaggaca gagatagaca	2148		
141	tgagctttga caacaatctg taggctctcc tgcttttagaa taagcatgta ccattcttta	2208		
143	tccattcccc ttattcctac atcaattgtt tttactttct tgggtgtgag actgagttag	2268		

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Output Set: N:\CRF4\11212002\I602597A.raw

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147 catgggcaga gagggccctg gatctcatcc agcccactcc ttttcccctt ccagtacagt 2388
149 gacactctgg tgcccattgg cagatggcga cttccctgca cccataactg atgctttgtg 2448
151 aattcttctt ccttttcaga actactctgt gctaattgtt ctgccagtat gggcgcatca 2508
153 gctccatcct gacaaacaag acatttaggt aaaactttgt aggcaccttc tgcttctctg 2568
155 cttcattgtt cctgtgatag tcctgtttgtt attacagcat gtacccaaaa cagcctcaca 2628
157 ttgttacagg aggcaggcca ggacatcaaa gtcatcatct ttatgtggca tgactcttaa 2688
159 gaggccatta ctgtatctca tggcctcttg atgtggaaag aagttgacag agggttgcag 2748
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167 <211> LENGTH: 254
168 <212> TYPE: PRT
169 <213> ORGANISM: Homo sapiens
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177 Ser Glu Ala Glu Leu Asp Glu Arg Arg Lys Arg Arg Gln Glu Glu Trp
178 20 25 30
181 Glu Lys Val Arg Lys Pro Glu Asp Pro Glu Glu Cys Pro Glu Glu Val
182 35 40 45
185 Tyr Asp Pro Arg Ser Leu Tyr Glu Arg Leu Gln Glu Gln Lys Asp Arg
186 50 55 60
189 Lys Gln Gln Glu Tyr Glu Glu Gln Phe Lys Phe Lys Asn Met Val Arg
190 65 70 75 80
193 Gly Leu Asp Glu Asp Glu Thr Asn Phe Leu Asp Glu Val Ser Arg Gln
194 85 90 95
197 Gln Glu Leu Ile Glu Lys Gln Arg Arg Glu Glu Glu Leu Lys Glu Leu
198 100 105 110
201 Lys Glu Tyr Arg Asn Asn Leu Lys Lys Val Gly Ile Ser Gln Glu Asn
202 115 120 125
205 Lys Lys Glu Val Glu Lys Lys Leu Thr Val Lys Pro Ile Glu Thr Lys
206 130 135 140
209 Asn Lys Phe Ser Gln Ala Lys Leu Leu Ala Gly Ala Val Lys His Lys
210 145 150 155 160
213 Ser Ser Glu Ser Gly Asn Ser Val Lys Arg Leu Lys Pro Asp Pro Glu
214 165 170 175
217 Pro Asp Asp Lys Asn Gln Glu Pro Ser Ser Cys Lys Ser Leu Gly Asn
218 180 185 190
221 Thr Ser Leu Ser Gly Pro Ser Ile His Cys Pro Ser Ala Ala Val Cys
222 195 200 205
225 Ile Gly Ile Leu Pro Gly Leu Gly Ala Tyr Ser Gly Ser Ser Asp Ser
226 210 215 220
229 Glu Ser Ser Ser Asp Ser Glu Gly Thr Ile Asn Ala Thr Gly Lys Ile
230 225 230 235 240
233 Val Ser Ser Ile Phe Arg Thr Asn Thr Phe Leu Glu Ala Pro
234 245 250
237 <210> SEQ ID NO: 3
238 <211> LENGTH: 1516

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Output Set: N:\CRF4\11212002\I602597A.raw

239 <212> TYPE: DNA

240 <213> ORGANISM: Homo sapiens

242 <220> FEATURE:

243 <221> NAME/KEY: CDS

244 <222> LOCATION: (101)..(649)

245 <223> OTHER INFORMATION:

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252                                     Met Ala Glu Phe Pro
253                                     1           5
255 tcg aaa gtt agc acg cgg acc agc agt cct gcg cag ggc gcc gaa gcc      163
256 Ser Lys Val Ser Thr Arg Thr Ser Ser Pro Ala Gln Gly Ala Glu Ala
257                                     10           15           20
259 tcg gtg tcg gcg ctg cgc ccg gac ctg ggc ttc gtg cgc tcc cgc ctc      211
260 Ser Val Ser Ala Leu Arg Pro Asp Leu Gly Phe Val Arg Ser Arg Leu
261                                     25           30           35
263 ggg gcg ctc atg ctg ctg cag ctg gtg ctg ggg ctg ctg gtg tgg gcg      259
264 Gly Ala Leu Met Leu Leu Gln Leu Val Leu Gly Leu Leu Val Trp Ala
265                                     40           45           50
267 ctg att gcg gac acc ccg tac cac ctg tat ccg gcc tat ggc tgg gtg      307
268 Leu Ile Ala Asp Thr Pro Tyr His Leu Tyr Pro Ala Tyr Gly Trp Val
269                                     55           60           65
271 atg ttc gtc gct gtc ttc ctc tgg ctg gtg aca atc gtc ctc ttc aac      355
272 Met Phe Val Ala Val Phe Leu Trp Leu Val Thr Ile Val Leu Phe Asn
273 70                                     75           80           85
275 ctc tac ctg ttt cag ctg cac atg aag ttg tac atg gtt ccc tgg cca      403
276 Leu Tyr Leu Phe Gln Leu His Met Lys Leu Tyr Met Val Pro Trp Pro
277                                     90           95           100
279 ctg gtg tta atg atc ttt aac atc agc gcc acc gtt ctc tac atc acc      451
280 Leu Val Leu Met Ile Phe Asn Ile Ser Ala Thr Val Leu Tyr Ile Thr
281                                     105          110          115
283 gcc ttc atc gcc tgc tct gcg gca gtt gac ctg aca tcc ctg agg ggc      499
284 Ala Phe Ile Ala Cys Ser Ala Ala Val Asp Leu Thr Ser Leu Arg Gly
285                                     120          125          130
287 acc cgg cct tat aac cag cgc gcg gct gcc tcg ttc ttt gcg tgt ttg      547
288 Thr Arg Pro Tyr Asn Gln Arg Ala Ala Ala Ser Phe Phe Ala Cys Leu
289                                     135          140          145
291 gtg atg atc gcc tat gga gtg agt gcc ttc ttc agc tac cag gcc tgg      595
292 Val Met Ile Ala Tyr Gly Val Ser Ala Phe Phe Ser Tyr Gln Ala Trp
293 150                                     155          160          165
295 cga gga gta ggc agc aat gcg gcc acc agt cag atg gct ggc ggc tat      643
296 Arg Gly Val Gly Ser Asn Ala Ala Thr Ser Gln Met Ala Gly Gly Tyr
297                                     170          175          180
299 gcc taa accacctgtg ccacggcccc ctctggggct gaagccgccg ctgggtcaca      699
300 Ala
303 gagcagggtc accctgcaag cctgaagctg gggagccctg cgtggagtca gcccaacagg      759
305 gactgcattt gctcctctct gcccgtcaga cataagctct cacagcgcta aggaagcagg      819
307 cccaggctgg caggcatctc ggcttgagg aggccaactg ctgagacctc ttctccatcc      879

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313 actccagacc tgcagcccca gaccgcgcgt agtataagcc taacaagcaa cacgtagcac 1059
315 cttagtcttt gttccaggag agctgagcaa gctggtgaaa ccactctcct tccttttaaac 1119
317 accgtttcaa ccaacctctc cctggagcca acctgtaaaa agtgggttga ttgctgacag 1179
319 catggctctc cctccctgca ttccagacat accagttact gaaagcaaat cagttttaag 1239
321 tgattttctca gtgctgaaaa gcctgtccag gtttctctcc ctttcccaag cctctctctg 1299
323 taatactccc tttgggcgaa gctaacatcg gtgcctcccc gaccttgctg actaggcaca 1359
325 tgggacgcaa aggagggagg gaagcaaggc cttgcctggc gagttgtcat gtggttggtg 1419
327 gtgactgttt tatttttttt aataaaaaata aagatgagag aaattaaaaa aaaaaaaaaa 1479
329 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1516

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332 <210> SEQ ID NO: 4

333 <211> LENGTH: 182

334 <212> TYPE: PRT

335 <213> ORGANISM: Homo sapiens

337 <400> SEQUENCE: 4

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344 20 25 30
347 Val Arg Ser Arg Leu Gly Ala Leu Met Leu Leu Gln Leu Val Leu Gly
348 35 40 45
351 Leu Leu Val Trp Ala Leu Ile Ala Asp Thr Pro Tyr His Leu Tyr Pro
352 50 55 60
355 Ala Tyr Gly Trp Val Met Phe Val Ala Val Phe Leu Trp Leu Val Thr
356 65 70 75 80
359 Ile Val Leu Phe Asn Leu Tyr Leu Phe Gln Leu His Met Lys Leu Tyr
360 85 90 95
363 Met Val Pro Trp Pro Leu Val Leu Met Ile Phe Asn Ile Ser Ala Thr
364 100 105 110
367 Val Leu Tyr Ile Thr Ala Phe Ile Ala Cys Ser Ala Ala Val Asp Leu
368 115 120 125
371 Thr Ser Leu Arg Gly Thr Arg Pro Tyr Asn Gln Arg Ala Ala Ala Ser
372 130 135 140
375 Phe Phe Ala Cys Leu Val Met Ile Ala Tyr Gly Val Ser Ala Phe Phe
376 145 150 155 160
379 Ser Tyr Gln Ala Trp Arg Gly Val Gly Ser Asn Ala Ala Thr Ser Gln
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383 Met Ala Gly Gly Tyr Ala

384 180

387 <210> SEQ ID NO: 5

388 <211> LENGTH: 2177

389 <212> TYPE: DNA

390 <213> ORGANISM: Homo sapiens

392 <220> FEATURE:

393 <221> NAME/KEY: CDS

394 <222> LOCATION: (167)..(1060)

395 <223> OTHER INFORMATION:

W--> 398 <400> 5

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/602,597A

DATE: 11/21/2002
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:7; N Pos. 5